

SEQUENCE LISTING

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Merkins, Louise
Bennett, Robert
Seiss, Donald

<120> Mammalian DNA Binding Membrane-Associated Protein-encoding Gene and Uses

<130> 00-617-A

<140> US 09/921,099

<141> 2001-08-01

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<170> PatentIn version 3.0

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Glu Leu Gln Ser Asp Tyr Thr Glu Asp Ala Thr Asp Thr Lys Pro

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Asp Arg 1055	Asp Ile Glu Leu Glu 1060	Leu Ser Ala Leu Asp Thr Asp Glu 1065
Pro Asp 1070	Gly Gln Ser Glu Pro 1075	Ile Glu Glu Ile Leu Asp Ile Gln 1080
Leu Gly 1085	Ile Ser Ser Gln Asn 1090	Asp Gln Leu Leu Asn Gly Met Ala 1095
Val Glu 1100	Asn Gly His Pro Val 1105	Gln Gln His Gln Lys Glu Pro Pro 1110
Lys Gln 1115	Lys Lys Gln Ser Leu 1120	Gly Glu Asp His Val Ile Leu Glu 1125
Glu Gln 1130	Lys Thr Ile Leu Pro 1135	Val Thr Ser Cys Phe Ser Gln Pro 1140
Leu Pro 1145	Val Ser Ile Ser Asn 1150	Ala Ser Cys Leu Pro Ile Thr Thr 1155
Ser Val 1160	Ser Ala Gly Asn Leu 1165	Ile Leu Lys Thr His Val Met Ser 1170
Glu Asp 1175	Lys Asn Asp Phe Leu 1180	Lys Pro Val Ala Asn Gly Lys Met 1185
Val Asn 1190	Ser	

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tattatgttt tggggtactg gttatccaag ggaaacactt ttttaaaca caaaacaaaa	180
aaaccgcccc gcagtccaaa gtaatttgtg ttcctaaaaa tggaatatgg aaagttaatt	240
tgcttggttg atgtggtcgt tgagaaaaat acataaaagc tttgatgttt attatgtgag	300
caaccaatat aaatacagtt tagttgaaag gaacactatt aaggtattgt ttccaggcag	360
aatttcagaa atgtaattaa ttcagcaa at aggtttttta aaaaagacat ccaaaggta	420
taaaattatt tagaagtatt ttaggtctga agctgtaata gttgacttaa gcaattaact	480
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aaacactaca cagcaaaata atgatctgct agactgctaa cccgagcatc cagcttccac	600
a atg gct gtg cag gca gct caa tgg aca gaa ttt ctg tcc tgt cca atc	649
Met Ala Val Gln Ala Ala Gln Trp Thr Glu Phe Leu Ser Cys Pro Ile	
1 5 10 15	
tgc tat aat gaa ttt gat gag aat gtg cac aaa ccc atc agt tta ggt	697
Cys Tyr Asn Glu Phe Asp Glu Asn Val His Lys Pro Ile Ser Leu Gly	
20 25 30	
tgt tca cac act gtt tgc aag acc tgc ttg aat aaa ctt cat cga aaa	745
Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys	
35 40 45	
gct tgt cct ttt gac cag act gcc atc aac aca gat att gat gta ctt	793
Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu	
50 55 60	
cct gtc aac ttc gca ctt ctc cag tta gtt gga gcc cag gta cca gat	841
Pro Val Asn Phe Ala Leu Leu Gln Leu Val Gly Ala Gln Val Pro Asp	
65 70 75 80	
cat cag tca att aag tta agt aat cta ggt gag aat aaa cac tat gag	889
His Gln Ser Ile Lys Leu Ser Asn Leu Gly Glu Asn Lys His Tyr Glu	
85 90 95	
gtt gca aag aaa tgc gtt gag gat ttg gca ctc tac tta aaa cca cta	937
Val Ala Lys Lys Cys Val Glu Asp Leu Ala Leu Tyr Leu Lys Pro Leu	
100 105 110	
agt gga ggt aaa ggt gta gct agc ttg aac cag agt gca ctg agc cgt	985
Ser Gly Gly Lys Gly Val Ala Ser Leu Asn Gln Ser Ala Leu Ser Arg	
115 120 125	
cca atg caa agg aaa ctg gtg aca ctt gta aac tgt caa ctg gtg gag	1033
Pro Met Gln Arg Lys Leu Val Thr Leu Val Asn Cys Gln Leu Val Glu	
130 135 140	
gaa gaa ggt cgt gta aga gcc atg cga gca gct cgt tcc ctt gga gaa	1081
Glu Glu Gly Arg Val Arg Ala Met Arg Ala Ala Arg Ser Leu Gly Glu	
145 150 155 160	
aga act gta aca gaa ctg ata tta cag cac cag aac cct cag cag ttg	1129

Arg Thr Val Thr Glu Leu Ile Leu Gln His Gln Asn Pro Gln Gln Leu	
165 170 175	
tct gcc aat cta tgg gcc gct gtc agg gct cga gga tgc cag ttt tta	1177
Ser Ala Asn Leu Trp Ala Ala Val Arg Ala Arg Gly Cys Gln Phe Leu	
180 185 190	
ggg cca gct atg caa gaa gag gcc ttg aag ctg gtg tta ctg gca tta	1225
Gly Pro Ala Met Gln Glu Glu Ala Leu Lys Leu Val Leu Leu Ala Leu	
195 200 205	
gaa gat ggt tct gcc ctc tca agg aaa gtt ctg gta ctt ttt gtt gtg	1273
Glu Asp Gly Ser Ala Leu Ser Arg Lys Val Leu Val Leu Phe Val Val	
210 215 220	
cag aga cta gaa cca aga ttt cct cag gca tca aaa aca agt att ggt	1321
Gln Arg Leu Glu Pro Arg Phe Pro Gln Ala Ser Lys Thr Ser Ile Gly	
225 230 235 240	
cat gtt gtg caa cta ctg tat cga gct tct tgt ttt aag gtt acc aaa	1369
His Val Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Lys Val Thr Lys	
245 250 255	
aga gat gaa gac tct tcc cta atg cag ctg aag gag gaa ttt cgg agt	1417
Arg Asp Glu Asp Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Ser	
260 265 270	
tat gaa gca tta cgc aga gaa cat gat gcc caa att gtt cat att gcc	1465
Tyr Glu Ala Leu Arg Arg Glu His Asp Ala Gln Ile Val His Ile Ala	
275 280 285	
atg gaa gca gga ctc cgt att tca cct gaa cag tgg tcc tct ctt ttg	1513
Met Glu Ala Gly Leu Arg Ile Ser Pro Glu Gln Trp Ser Ser Leu Leu	
290 295 300	
tat ggt gat ttg gct cat aaa tca cac atg cag tct atc att gat aag	1561
Tyr Gly Asp Leu Ala His Lys Ser His Met Gln Ser Ile Ile Asp Lys	
305 310 315 320	
cta cag tct cca gag tca ttt gca aag agt gtc cag gaa ttg aca att	1609
Leu Gln Ser Pro Glu Ser Phe Ala Lys Ser Val Gln Glu Leu Thr Ile	
325 330 335	
gtt ttg caa cga aca ggt gac cca gct aac tta aat aga ctg agg cct	1657
Val Leu Gln Arg Thr Gly Asp Pro Ala Asn Leu Asn Arg Leu Arg Pro	
340 345 350	
cat tta gag ctt ctt gca aac ata gac cct aat cca gac gct gtt tca	1705
His Leu Glu Leu Leu Ala Asn Ile Asp Pro Asn Pro Asp Ala Val Ser	
355 360 365	
cca act tgg gag cag ctg gaa aat gca atg gta gct gtt aaa aca gta	1753
Pro Thr Trp Glu Gln Leu Glu Asn Ala Met Val Ala Val Lys Thr Val	
370 375 380	
gtt cat ggc ctt gtg gac ttc ata caa aat tat agt aga aaa ggc cat	1801
Val His Gly Leu Val Asp Phe Ile Gln Asn Tyr Ser Arg Lys Gly His	

385	390	395	400	
gag acc cct cag cct cag cca aac agc aaa tac aag act agc atg tgc				1849
Glu Thr Pro Gln Pro Gln Pro Asn Ser Lys Tyr Lys Thr Ser Met Cys	405	410	415	
cga gat ttg cga cag cag ggg ggt tgt cca cga gga aca aat tgt aca				1897
Arg Asp Leu Arg Gln Gln Gly Gly Cys Pro Arg Gly Thr Asn Cys Thr	420	425	430	
ttt gcc cat tct cag gaa gag ctt gaa aag tat cga tta agg aac aaa				1945
Phe Ala His Ser Gln Glu Glu Leu Glu Lys Tyr Arg Leu Arg Asn Lys	435	440	445	
aag atc aat gcc act gta aga acg ttt cct ctt cta aat aaa gtt ggt				1993
Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly	450	455	460	
gta aac aac act gtc aca acc aca gcc gga aat gtc att tct gtc ata				2041
Val Asn Asn Thr Val Thr Thr Thr Ala Gly Asn Val Ile Ser Val Ile	465	470	475	480
gga agt act gaa aca aca ggg aaa att gtt cca agt aca aac gga att				2089
Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile	485	490	495	
tca aat gca gaa aac agt gtt tcc cag cta atc tca cgt agt act gac				2137
Ser Asn Ala Glu Asn Ser Val Ser Gln Leu Ile Ser Arg Ser Thr Asp	500	505	510	
agt acc tta aga gct ctg gag acc gtg aag aaa gtg gga aag gtt ggc				2185
Ser Thr Leu Arg Ala Leu Glu Thr Val Lys Lys Val Gly Lys Val Gly	515	520	525	
gct aat ggt cag aat gct gct ggg ccc tct gca gat tct gta act gaa				2233
Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu	530	535	540	
aat aaa att ggt tct cca ccc aag act cct gta agt aat gta gca gct				2281
Asn Lys Ile Gly Ser Pro Pro Lys Thr Pro Val Ser Asn Val Ala Ala	545	550	555	560
acc tca gct ggg ccc tct aat gtt gga aca gag ctg aat tct gtg cct				2329
Thr Ser Ala Gly Pro Ser Asn Val Gly Thr Glu Leu Asn Ser Val Pro	565	570	575	
caa aaa tcc agc cca ttt cta act aga gta cca gta tat cct ccg cat				2377
Gln Lys Ser Ser Pro Phe Leu Thr Arg Val Pro Val Tyr Pro Pro His	580	585	590	
tct gaa aac att cag tat ttt caa gat cca agg act cag ata ccc ttt				2425
Ser Glu Asn Ile Gln Tyr Phe Gln Asp Pro Arg Thr Gln Ile Pro Phe	595	600	605	
gaa gtc cca cag tac cca cag aca gga tac tat cca cca cct cca acg				2473
Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr	610	615	620	

gta cca gct ggt gtg gct ccc tgt gtt cct cgc ttt gtg agg tcc aat Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn 625 630 635 640	2521
aac gtt cca gag tcc tcc ctc cca cct gct tcc atg cca tat gcc gat Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp 645 650 655	2569
cat tac agt aca ttt tcc cct cga gat cga atg aat tct tct cct tac His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr 660 665 670	2617
cag cct cct cct ccg cag ccg tat gga cca gtt cct cca gta cct tct Gln Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser 675 680 685	2665
gga atg tat gct cct gtg tac gac agc agg cgc atc tgg cgc cca cct Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro 690 695 700	2713
atg tac caa cga gat gac att att aga agc aat tct tta cct cca atg Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met 705 710 715 720	2761
gat gtg atg cac tca tct gtc tat cag aca tct ttg cgg gaa aga tat Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr 725 730 735	2809
aac tca tta gat gga tat tat tcg gtg gct tgt cag cca cca agt gag Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu 740 745 750	2857
cca agg aca act gtg cct tta cca agg gaa cct tgt ggt cat ttg aag Pro Arg Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys 755 760 765	2905
acc agt tgc gag gag cag ata aga aga aag cca gat cag tgg gca cag Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln 770 775 780	2953
tac cac act cag aaa gca cct ctt gtc tct tca act ctt cct gtg gca Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala 785 790 795 800	3001
aca cag tca cca aca cca cct tct cct ctg ttc agt gta gac ttt cgt Thr Gln Ser Pro Thr Pro Pro Ser Pro Leu Phe Ser Val Asp Phe Arg 805 810 815	3049
gcg gat ttc tca gag agt gtg agt ggt aca aaa ttt gaa gaa gat cat Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His 820 825 830	3097
ctt tcc cat tat tct ccc tgg tct tgt ggc acc ata ggc tcc tgt ata Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile 835 840 845	3145

aat gcc att gat tca gag ccc aaa gat gtc att gct aat tca aat gct Asn Ala Ile Asp Ser Glu Pro Lys Asp Val Ile Ala Asn Ser Asn Ala 850 855 860	3193
gtg tta atg gac ctg gac agt ggt gat gtt aag aga aga gta cat tta Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu 865 870 875 880	3241
ttt gaa acc cag aga agg aca aaa gaa gaa gat cca ata att ccc ttt Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe 885 890 895	3289
agt gat gga ccc atc atc tca aaa tgg ggt gcg att tcc aga tct tcc Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser 900 905 910	3337
cgt aca ggt tac cat acc aca gat cct gtc cag gcc act gct tcc caa Arg Thr Gly Tyr His Thr Thr Asp Pro Val Gln Ala Thr Ala Ser Gln 915 920 925	3385
gga agt gcg act aag ccc atc agt gta tca gat tat gtc cct tat gtc Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val 930 935 940	3433
aat gct gtt gat tca agg tgg agt tca tat ggc aac gag gcc aca tca Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser 945 950 955 960	3481
tca gca cac tat gtt gaa agg gac aga ttc att gtt act gat tta tct Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser 965 970 975	3529
ggt cat aga aag cat tcc agt act ggg gac ctt ttg agc ctt gaa ctt Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu 980 985 990	3577
cag cag gcc aag agc aac tca tta ctt ctt cag aga gag gcc aat gct Gln Gln Ala Lys Ser Asn Ser Leu Leu Leu Gln Arg Glu Ala Asn Ala 995 1000 1005	3625
ttg gcc atg caa cag aag tgg aat tcc ctg gat gaa ggc cgt cac Leu Ala Met Gln Gln Lys Trp Asn Ser Leu Asp Glu Gly Arg His 1010 1015 1020	3670
ctt acc tta aac ctt tta agc aag gaa att gaa cta aga aat gga Leu Thr Leu Asn Leu Leu Ser Lys Glu Ile Glu Leu Arg Asn Gly 1025 1030 1035	3715
gag tta cag agt gat tat aca gaa gat gca aca gat act aaa cct Glu Leu Gln Ser Asp Tyr Thr Glu Asp Ala Thr Asp Thr Lys Pro 1040 1045 1050	3760
gat agg gat atc gag tta gag ctt tca gca ctt gat act gat gaa Asp Arg Asp Ile Glu Leu Glu Leu Ser Ala Leu Asp Thr Asp Glu 1055 1060 1065	3805
cct gat gga caa agt gaa cca att gaa gag atc ttg gac ata cag	3850

Pro Asp Gly Gln Ser Glu Pro Ile Glu Glu Ile Leu Asp Ile Gln	
1070 1075 1080	
ctt ggt atc agt tct caa aat gat cag ttg cta aat gga atg gca	3895
Leu Gly Ile Ser Ser Gln Asn Asp Gln Leu Leu Asn Gly Met Ala	
1085 1090 1095	
gtg gaa aat ggg cat cca gta cag cag cac caa aag gag cca cca	3940
Val Glu Asn Gly His Pro Val Gln Gln His Gln Lys Glu Pro Pro	
1100 1105 1110	
aag cag aag aaa cag agt tta ggt gaa gac cat gtg att ctg gag	3985
Lys Gln Lys Lys Gln Ser Leu Gly Glu Asp His Val Ile Leu Glu	
1115 1120 1125	
gag caa aaa aca att ctg ccg gta act tct tgc ttt agc cag cca	4030
Glu Gln Lys Thr Ile Leu Pro Val Thr Ser Cys Phe Ser Gln Pro	
1130 1135 1140	
ctc cca gtg tct att agc aat gca agt tgc ctc ccc atc acc aca	4075
Leu Pro Val Ser Ile Ser Asn Ala Ser Cys Leu Pro Ile Thr Thr	
1145 1150 1155	
tct gtc agt gct ggc aac ctc att ctg aaa act cat gtt atg tct	4120
Ser Val Ser Ala Gly Asn Leu Ile Leu Lys Thr His Val Met Ser	
1160 1165 1170	
gaa gat aaa aac gac ttt tta aaa cct gtt gca aat ggg aag atg	4165
Glu Asp Lys Asn Asp Phe Leu Lys Pro Val Ala Asn Gly Lys Met	
1175 1180 1185	
gtt aac agc tgaaaggagg ttcattctttc aaatttgtga ccacaccatg	4214
Val Asn Ser	
1190	
gaagcattta cactagcttt ttatatatat aatatatatt atataatgta tatttttttt	4274
aaaaaaaaaga tattactggg ggcatccatt tcctgtggac tctttgatac ttcaagccct	4334
cttgcattag cattatg	4351

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<400> 4

Met Ala Val Gln Ala Ala Gln Trp Thr Glu Phe Leu Ser Cys Pro Ile
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Cys Tyr Asn Glu Phe Asp Glu Asn Val His Lys Pro Ile Ser Leu Gly
20 25 30

Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys
 35 40 45

Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu
 50 55 60

Pro Val Asn Phe Ala Leu Leu Gln Leu Val Gly Ala Gln Val Pro Asp
 65 70 75 80

His Gln Ser Ile Lys Leu Ser Asn Leu Gly Glu Asn Lys His Tyr Glu
 85 90 95

Val Ala Lys Lys Cys Val Glu Asp Leu Ala Leu Tyr Leu Lys Pro Leu
 100 105 110

Ser Gly Gly Lys Gly Val Ala Ser Leu Asn Gln Ser Ala Leu Ser Arg
 115 120 125

Pro Met Gln Arg Lys Leu Val Thr Leu Val Asn Cys Gln Leu Val Glu
 130 135 140

Glu Glu Gly Arg Val Arg Ala Met Arg Ala Ala Arg Ser Leu Gly Glu
 145 150 155 160

Arg Thr Val Thr Glu Leu Ile Leu Gln His Gln Asn Pro Gln Gln Leu
 165 170 175

Ser Ala Asn Leu Trp Ala Ala Val Arg Ala Arg Gly Cys Gln Phe Leu
 180 185 190

Gly Pro Ala Met Gln Glu Glu Ala Leu Lys Leu Val Leu Leu Ala Leu
 195 200 205

Glu Asp Gly Ser Ala Leu Ser Arg Lys Val Leu Val Leu Phe Val Val
 210 215 220

Gln Arg Leu Glu Pro Arg Phe Pro Gln Ala Ser Lys Thr Ser Ile Gly
 225 230 235 240

His Val Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Lys Val Thr Lys
 245 250 255

Arg Asp Glu Asp Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Ser

260

265

270

Tyr Glu Ala Leu Arg Arg Glu His Asp Ala Gln Ile Val His Ile Ala
275 280 285

Met Glu Ala Gly Leu Arg Ile Ser Pro Glu Gln Trp Ser Ser Leu Leu
290 295 300

Tyr Gly Asp Leu Ala His Lys Ser His Met Gln Ser Ile Ile Asp Lys
305 310 315 320

Leu Gln Ser Pro Glu Ser Phe Ala Lys Ser Val Gln Glu Leu Thr Ile
325 330 335

Val Leu Gln Arg Thr Gly Asp Pro Ala Asn Leu Asn Arg Leu Arg Pro
340 345 350

His Leu Glu Leu Leu Ala Asn Ile Asp Pro Asn Pro Asp Ala Val Ser
355 360 365

Pro Thr Trp Glu Gln Leu Glu Asn Ala Met Val Ala Val Lys Thr Val
370 375 380

Val His Gly Leu Val Asp Phe Ile Gln Asn Tyr Ser Arg Lys Gly His
385 390 395 400

Glu Thr Pro Gln Pro Gln Pro Asn Ser Lys Tyr Lys Thr Ser Met Cys
405 410 415

Arg Asp Leu Arg Gln Gln Gly Gly Cys Pro Arg Gly Thr Asn Cys Thr
420 425 430

Phe Ala His Ser Gln Glu Glu Leu Glu Lys Tyr Arg Leu Arg Asn Lys
435 440 445

Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly
450 455 460

Val Asn Asn Thr Val Thr Thr Thr Ala Gly Asn Val Ile Ser Val Ile
465 470 475 480

Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile
485 490 495

Ser Asn Ala Glu Asn Ser Val Ser Gln Leu Ile Ser Arg Ser Thr Asp
500 505 510

Ser Thr Leu Arg Ala Leu Glu Thr Val Lys Lys Val Gly Lys Val Gly
515 520 525

Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu
530 535 540

Asn Lys Ile Gly Ser Pro Pro Lys Thr Pro Val Ser Asn Val Ala Ala
545 550 555 560

Thr Ser Ala Gly Pro Ser Asn Val Gly Thr Glu Leu Asn Ser Val Pro
565 570 575

Gln Lys Ser Ser Pro Phe Leu Thr Arg Val Pro Val Tyr Pro Pro His
580 585 590

Ser Glu Asn Ile Gln Tyr Phe Gln Asp Pro Arg Thr Gln Ile Pro Phe
595 600 605

Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr
610 615 620

Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn
625 630 635 640

Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp
645 650 655

His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr
660 665 670

Gln Pro Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser
675 680 685

Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro
690 695 700

Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met
705 710 715 720

Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr
725 730 735

Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu
740 745 750

Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys
755 760 765

Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln
770 775 780

Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala
785 790 795 800

Thr Gln Ser Pro Thr Pro Pro Ser Pro Leu Phe Ser Val Asp Phe Arg
805 810 815

Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His
820 825 830

Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile
835 840 845

Asn Ala Ile Asp Ser Glu Pro Lys Asp Val Ile Ala Asn Ser Asn Ala
850 855 860

Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu
865 870 875 880

Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe
885 890 895

Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser
900 905 910

Arg Thr Gly Tyr His Thr Thr Asp Pro Val Gln Ala Thr Ala Ser Gln
915 920 925

Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val
930 935 940

Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser
 945 950 955 960

Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser
 965 970 975

Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu
 980 985 990

Gln Gln Ala Lys Ser Asn Ser Leu Leu Leu Gln Arg Glu Ala Asn Ala
 995 1000 1005

Leu Ala Met Gln Gln Lys Trp Asn Ser Leu Asp Glu Gly Arg His
 1010 1015 1020

Leu Thr Leu Asn Leu Leu Ser Lys Glu Ile Glu Leu Arg Asn Gly
 1025 1030 1035

Glu Leu Gln Ser Asp Tyr Thr Glu Asp Ala Thr Asp Thr Lys Pro
 1040 1045 1050

Asp Arg Asp Ile Glu Leu Glu Leu Ser Ala Leu Asp Thr Asp Glu
 1055 1060 1065

Pro Asp Gly Gln Ser Glu Pro Ile Glu Glu Ile Leu Asp Ile Gln
 1070 1075 1080

Leu Gly Ile Ser Ser Gln Asn Asp Gln Leu Leu Asn Gly Met Ala
 1085 1090 1095

Val Glu Asn Gly His Pro Val Gln Gln His Gln Lys Glu Pro Pro
 1100 1105 1110

Lys Gln Lys Lys Gln Ser Leu Gly Glu Asp His Val Ile Leu Glu
 1115 1120 1125

Glu Gln Lys Thr Ile Leu Pro Val Thr Ser Cys Phe Ser Gln Pro
 1130 1135 1140

Leu Pro Val Ser Ile Ser Asn Ala Ser Cys Leu Pro Ile Thr Thr
 1145 1150 1155

Ser Val Ser Ala Gly Asn Leu Ile Leu Lys Thr His Val Met Ser

1160

1165

1170

Glu Asp Lys Asn Asp Phe Leu Lys Pro Val Ala Asn Gly Lys Met
 1175 1180 1185

Val Asn Ser
 1190

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 <212> DNA
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 <223> PCR primer 1 for cloning DNA-R

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39

<210> 6
 <211> 26
 <212> DNA
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<220>
 <223> PCR primer 2 for cloning DNA-R

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26

<210> 7
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Met Ala Thr Leu Val Val Asn Lys Leu Gly Ala Gly Val Asp Ser Gly
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Arg Gln Gly Ser Arg Gly Thr Ala Val Val Lys Val Leu Glu Cys Gly
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Val Cys Glu Asp Val Phe Ser Leu Gln Gly Asp Lys Val Pro Arg Leu
 35 40 45

Leu Leu Cys Gly His Thr Val Cys His Asp Cys Leu Thr Arg Leu Pro
 50 55 60

Leu His Gly Arg Ala Ile Arg Cys Pro Phe Asp Arg Gln Val Thr Asp
 65 70 75 80

Leu Gly Asp Ser Gly Val Trp Gly Leu Lys Lys Asn Phe Ala Leu Leu
 85 90 95
 Glu Leu Leu Glu Arg Leu Gln Asn Gly Pro Ile Gly Gln Tyr Gly Ala
 100 105 110
 Ala Glu Glu Ser Ile Gly Ile Ser Gly Glu Ser Ile Ile Arg Cys Asp
 115 120 125
 Glu Asp Glu Ala His Leu Ala Ser Val Tyr Cys Thr Val Cys Ala Thr
 130 135 140
 His Leu Cys Ser Glu Cys Ser Gln Val Thr His Ser Thr Lys Thr Leu
 145 150 155 160
 Ala Lys His Arg Arg Val Pro Leu Ala Asp Lys Pro His Glu Lys Thr
 165 170 175
 Met Cys Ser Gln His Gln Val His Ala Ile Glu Phe Val Cys Leu Glu
 180 185 190
 Glu Gly Cys Gln Thr Ser Pro Leu Met Cys Cys Val Cys Lys Glu Tyr
 195 200 205
 Gly Lys His Gln Gly His Lys His Ser Val Leu Glu Pro Glu Ala Asn
 210 215 220
 Gln Ile Arg Ala Ser Ile Leu Asp Met Ala His Cys Ile Arg Thr Phe
 225 230 235 240
 Thr Glu Glu Ile Ser Asp Tyr Ser Arg Lys Leu Val Gly Ile Val Gln
 245 250 255
 His Ile Glu Gly Gly Glu Gln Ile Val Glu Asp Gly Ile Gly Met Ala
 260 265 270
 His Thr Glu His Val Pro Gly Thr Ala Glu Asn Ala Arg Ser Cys Ile
 275 280 285
 Arg Ala Tyr Phe Tyr Asp Leu His Glu Thr Leu Cys Arg Gln Glu Glu
 290 295 300
 Met Ala Leu Ser Val Val Asp Ala His Val Arg Glu Lys Leu Ile Trp
 305 310 315 320
 Leu Arg Gln Gln Gln Glu Asp Met Thr Ile Leu Leu Ser Glu Val Ser
 325 330 335
 Ala Ala Cys Leu His Cys Glu Lys Thr Leu Gln Gln Asp Asp Cys Arg
 340 345 350
 Val Val Leu Ala Lys Gln Glu Ile Thr Arg Leu Leu Thr Glu Leu Gln
 355 360 365
 Lys Gln Gln Gln Gln Phe Thr Glu Val Ala Asp His Ile Gln Leu Asp
 370 375 380

Ala Ser Ile Pro Val Thr Phe Thr Lys Asp Asn Arg Val His Ile Gly
385 390 395 400

Pro Lys Met Glu Ile Arg Val Val Thr Leu Gly Leu Asp Gly Ala Gly
405 410 415

Lys Thr Thr Ile Leu Phe Lys Leu Lys Gln Asp Glu Phe Met Gln Pro
420 425 430

Ile Pro Thr Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Leu
435 440 445

Lys Phe Thr Ile Trp Asp Val Gly Gly Lys His Lys Leu Arg Pro Leu
450 455 460

Trp Lys His Tyr Tyr Leu Asn Thr Gln Ala Val Val Phe Val Val Asp
465 470 475 480

Ser Ser His Arg Asp Arg Ile Ser Glu Ala His Ser Glu Leu Ala Lys
485 490 495

Leu Leu Thr Glu Lys Glu Leu Arg Asp Ala Leu Leu Leu Ile Phe Ala
500 505 510

Asn Lys Gln Asp Val Ala Gly Ala Leu Ser Val Glu Glu Ile Thr Glu
515 520 525

Leu Leu Ser Leu His Lys Leu Cys Cys Gly Arg Ser Trp Tyr Ile Gln
530 535 540

Gly Cys Asp Ala Arg Ser Gly Met Gly Leu Tyr Glu Gly Leu Asp Trp
545 550 555 560

Leu Ser Arg Gln Leu Val Ala Ala Gly Val Leu Asp Val Ala
565 570

<210> 8

<211> 317

<212> PRT

<213> Homo sapiens

<400> 8

Met Gly Tyr Asp Val Thr Arg Phe Gln Gly Asp Val Asp Glu Asp Leu
1 5 10 15

Ile Cys Pro Ile Cys Ser Gly Val Leu Glu Glu Pro Val Gln Ala Pro
20 25 30

His Cys Glu His Ala Phe Cys Asn Ala Cys Ile Thr Gln Trp Phe Ser
35 40 45

Gln Gln Gln Thr Cys Pro Val Asp Arg Ser Val Val Thr Val Ala His
50 55 60

Leu Arg Pro Val Pro Arg Ile Met Arg Asn Met Leu Ser Lys Leu Gln
65 70 75 80

Ile Ala Cys Asp Asn Ala Val Phe Gly Cys Ser Ala Val Val Arg Leu
 85 90 95
 Asp Asn Leu Met Ser His Leu Ser Asp Cys Glu His Asn Pro Lys Arg
 100 105 110
 Pro Val Thr Cys Glu Gln Gly Cys Gly Leu Glu Met Pro Lys Asp Glu
 115 120 125
 Leu Pro Asn His Asn Cys Ile Lys His Leu Arg Ser Val Val Gln Gln
 130 135 140
 Gln Gln Thr Arg Ile Ala Glu Leu Glu Lys Thr Ser Ala Glu His Lys
 145 150 155 160
 His Gln Leu Ala Glu Gln Lys Arg Asp Ile Gln Leu Leu Lys Ala Tyr
 165 170 175
 Met Arg Ala Ile Arg Ser Val Asn Pro Asn Leu Gln Asn Leu Glu Glu
 180 185 190
 Thr Ile Glu Tyr Asn Glu Ile Leu Glu Trp Val Asn Ser Leu Gln Pro
 195 200 205
 Ala Arg Val Thr Arg Trp Gly Gly Met Ile Ser Thr Pro Asp Ala Val
 210 215 220
 Leu Gln Ala Val Ile Lys Arg Ser Leu Val Glu Ser Gly Cys Pro Ala
 225 230 235 240
 Ser Ile Val Asn Glu Leu Ile Glu Asn Ala His Glu Arg Ser Trp Pro
 245 250 255
 Gln Gly Leu Ala Thr Leu Glu Thr Arg Gln Met Asn Arg Arg Tyr Tyr
 260 265 270
 Glu Asn Tyr Val Ala Lys Arg Ile Pro Gly Lys Gln Ala Val Val Val
 275 280 285
 Met Ala Cys Glu Asn Gln His Met Gly Asp Asp Met Val Gln Glu Pro
 290 295 300
 Gly Leu Val Met Ile Phe Ala His Gly Val Glu Glu Ile
 305 310 315

<210> 9
 <211> 202
 <212> PRT
 <213> Caenorhabditis elegans

<400> 9

Met Arg Met Met Glu Ala Glu Ile Lys Asp Gln Arg Asn Asn Leu Gln
 1 5 10 15
 Ala Leu Lys Asn Ser Gln Arg Leu Ser Val Arg Gly Ser Ile Gln Ser

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Asn Met Ser Ser Arg Thr Asp Gly Ile Leu Gln Arg Arg Leu Asp Glu		
35	40	45
Thr Glu Arg Lys Leu Ala Lys Thr Ser Ala Glu Leu Lys Ala Lys Asp		
50	55	60
Glu Lys Leu Lys Lys Glu Thr Ala Ser Leu Glu Ala Ser Arg Glu Ala		
65	70	75
His Arg Leu Leu Gln Glu Glu Ser Asn Lys Ser Lys Val Ser Val Met		
85	90	95
Arg Leu Thr Phe Lys Leu Asn Arg Ile Thr His Glu Ser Val Lys Glu		
100	105	110
Gln Ala Val Leu Lys Lys Lys Leu Leu Asp Cys Glu Thr Arg Leu Ala		
115	120	125
Thr Tyr Ser Glu Cys Leu Val Cys Tyr Gln Lys Phe Asp Glu Asn Thr		
130	135	140
Arg Ile Pro Arg Val Met Asp Cys Gly His Thr Leu Cys Asp Phe Cys		
145	150	155
Ile Asn Gln Ile Val Lys Met Ala Gly Cys Tyr Ser Ala Thr Cys Pro		
165	170	175
Phe Asp Arg Val Arg Ile Phe Gly Phe Gly Lys Ser Arg Arg Leu Glu		
180	185	190
Asp Arg Pro Cys Asn Arg Phe Ile Met Lys		
195	200	
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<211> 218		
<212> PRT		
<213> Caenorhabditis elegans		
<400> 10		
Met Ala Pro Ile Arg Arg Ser Ser Arg Leu Ala Glu Arg Tyr Asp Ala		
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Ile Glu Ser Lys Lys Arg Ser Leu Lys Arg Leu Glu Glu Gln Ile Lys		
20	25	30
Ala Glu Glu Glu Gln Phe Ser Asp Lys Met Lys Gln Leu Glu Asp Glu		
35	40	45
Ile Lys Ile Lys Glu Gln Val Ile Thr Met Phe Lys Arg Lys Thr Val		
50	55	60
Arg Arg Glu Trp Met Arg Asn Ser Arg Gln Ala Thr Thr Asn Ile Asn		
65	70	75
		80

Ile Ala Gln Ile Glu Ser Leu Lys Leu Gln Leu Glu Glu Gly Glu Lys
85 90 95

Asp Ile Ala Glu Ala Glu Lys Gln Ala Glu Pro Thr Thr Pro Gln Gln
100 105 110

Glu Ala Glu Leu Ser Glu Thr Phe Lys Gln Met Val Arg Asp Arg Met
115 120 125

Lys Val Lys Asp Val Asp Glu Lys Leu Leu Gln Gln Tyr Met Lys Lys
130 135 140

Glu Asn Val Glu Phe Glu Trp Arg Ser Cys Phe Ile Cys Thr Met Glu
145 150 155 160

Tyr Ser Arg Thr Asp Lys Asn Leu His Pro Ile Ile Leu Asn Cys Gly
165 170 175

His Asn Leu Cys Arg Ser Cys Ile Asn Lys Leu Thr Gly Asn Gly Ile
180 185 190

Val Lys Cys Pro Phe Asp Arg Leu Asp Thr Arg Val Arg Val Thr Gly
195 200 205

Leu Pro Arg Asn Leu Ala Leu Ile Asn Leu
210 215

<210> 11

<211> 1048

<212> PRT

<213> Caenorhabditis elegans

<400> 11

Met Ala Pro Thr Gly Gln Gly Gly Gln Trp Gln Glu Val Leu Cys Cys
1 5 10 15

Ser Ile Cys Asn Arg His Phe Asn Glu Thr Phe Leu Pro Val Ser Leu
20 25 30

Ile Cys Gly His Val Ile Cys Arg Lys Cys Ala Glu Lys Pro Glu Asn
35 40 45

Gln Thr Lys Pro Cys Pro His Asp Asp Trp Lys Thr Thr His Ser Pro
50 55 60

Ser Glu Tyr Pro Asn Asn Val Ala Leu Leu Ser Val Ile Phe Pro Arg
65 70 75 80

Lys Gln Cys Met Thr Leu Ser Gly Ala Val Ser Glu Ala Glu Lys Arg
85 90 95

Val Asp Gln Leu Ser Ile Gln Ile Ala Lys Phe Phe Arg Glu Ala Asp
100 105 110

Ser Glu Arg Gly Gly Thr Val Ser Ser Arg Glu Ile Ser Arg Thr Leu
115 120 125

Gln Arg Lys Val Leu Ala Leu Leu Cys Tyr Gln Trp Arg Glu Val Asp
 130 135 140
 Gly Arg Leu Lys Thr Leu Lys Met Cys Arg Gly Ile Ser Glu Arg Val
 145 150 155 160
 Met Ile Glu Ile Ile Leu Ser Ile Gln Ser Asn Thr His Val Ser Ser
 165 170 175
 Gln Leu Trp Ser Ala Val Arg Ala Arg Gly Cys Gln Phe Leu Gly Pro
 180 185 190
 Ala Met Gln Asp Asp Val Leu Arg Leu Ile Leu Met Thr Leu Glu Thr
 195 200 205
 Gly Glu Cys Ile Ala Arg Lys Asn Leu Val Met Tyr Val Val Gln Thr
 210 215 220
 Leu Ala Ser Asp Tyr Pro Gln Val Ser Lys Thr Cys Val Gly His Val
 225 230 235 240
 Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Asn Val Leu Lys Arg Asp
 245 250 255
 Gly Glu Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Thr Tyr Glu
 260 265 270
 Ser Leu Arg Arg Glu His Asp Ser Gln Ile Val Gln Ile Ala Phe Glu
 275 280 285
 Ser Gly Leu Arg Ile Gly Pro Asp Gln Trp Ser Ala Leu Leu Tyr Ala
 290 295 300
 Asp Gln Ser His Arg Ser His Met Gln Ser Ile Ile Asp Lys Leu Gln
 305 310 315 320
 Ser Lys Asn Ser Tyr Gln Gln Gly Val Glu Glu Leu Arg Ala Leu Ala
 325 330 335
 Gly Ser Gln Thr Ser Met Leu Val Pro Ala Tyr Arg Tyr Phe Leu Thr
 340 345 350
 Gln Val Ile Pro Cys Leu Glu Phe Phe Ala Gly Ile Glu His Glu Asp
 355 360 365
 Thr Ser Met Arg Met Ile Gly Asp Ala Leu His Gln Ile Arg Ile Leu
 370 375 380
 Leu Lys Leu His Cys Ser Gln Asp Asp Leu Arg Lys Met Pro Lys Glu
 385 390 395 400
 Glu Arg Arg Gly Val Ile Leu Gln Ala Glu Val Pro Gly Gly Met Gly
 405 410 415
 Gly Gly Pro Gly Gly Ser Gly Gly Ala Glu Ala Gly Arg Ile Gly Gly
 420 425 430

Leu His Pro Leu Tyr Ser Gln Ile Asp Glu Thr Gly Arg Ser Ile Ser
 435 440 445

Arg Thr Asn Pro Lys Asp Asn Ser His Asn Ser Pro Gln Thr Pro Pro
 450 455 460

Lys Gln Pro Arg Gln Lys Arg Tyr Gln Met Gly Ile Pro Pro Asn Arg
 465 470 475 480

Met Gly Tyr Ser Ser Asp Ala Pro Pro Phe Ile Pro Ser His Gln Gln
 485 490 495

Gln Pro Pro Pro Gln Phe Phe Asn Ser Gln His Leu Pro Gln Arg Phe
 500 505 510

Arg Gly Gly Arg Gln Arg Gly Ala Pro Pro Pro Pro Pro Gln Pro
 515 520 525

Met Pro Met Leu Ile Gly Tyr Asp Met Pro Gly Ala Pro Met Met Gln
 530 535 540

Ala Thr Glu Val Leu Thr Ala Asp Gly Gln Met Val Asn Gly Thr Pro
 545 550 555 560

Gln Arg Val Val Ile Met Gln Ser Pro Thr His Leu Pro Gly Gly Pro
 565 570 575

Val Val Met Ile Pro Gln Gln Gln Met Val Pro Pro Pro Gln Ser Met
 580 585 590

Thr Pro Val Gly Gly Pro Met Gly Pro Met Gly Pro Met Thr Pro Ser
 595 600 605

Ile Pro Val Gln Val Pro Pro Asn Thr Met Trp Thr Ala Thr Ser Pro
 610 615 620

Thr Gly Ser Val Ile Tyr Pro Ala Ala Ser Pro Pro Gly Gln Pro Pro
 625 630 635 640

His Thr Ile Trp Ile Gln Ser Ile Gly Val Phe Lys Arg Lys Ser Asn
 645 650 655

Phe Leu Lys Ile Val Arg Lys Ile Ser Phe Phe Leu Asn Phe Tyr Asp
 660 665 670

Phe Phe Leu Ile Leu Arg Lys Leu Lys Lys Glu Lys Lys Gly Ala Asp
 675 680 685

Ile Glu Phe Phe Glu Lys Ile Lys Ser Thr Asp Phe Lys Lys Tyr Pro
 690 695 700

Ser Ser Phe Ser Arg Thr Asp Gly Asn Met Phe Pro Met Phe Asp Arg
 705 710 715 720

Gly Ser Gly Gly Met Val Trp Gly Pro Gly Thr Met Leu Arg Glu Ser
 725 730 735

Gly Ala Asp Ala Glu Gln Leu Leu Ala Lys Arg Tyr Glu Ile Leu Lys
 740 745 750
 Arg Leu Gln Pro Ser Glu Asp Asp Asp Asp Pro Glu Asp Gly Gly Ile
 755 760 765
 Gly His Val Ser Tyr Thr Val Ala Ser Ser Val Leu Asp Asp Arg Met
 770 775 780
 Asp His His Pro Leu Thr Met Ile Pro Val Pro Thr Ile Asp Leu Pro
 785 790 795 800
 Ala Ile Pro Ile Ser Phe Ala Asn Met Pro Thr Glu Glu Thr Met Thr
 805 810 815
 Met Ile Gly Glu Met Val Gln Asn Arg Pro Arg Ala Pro Ser Leu Thr
 820 825 830
 Ala Pro Ser Ser Asn Gln Pro Met Asn Val Asn Ala Ser Ala Ser Ala
 835 840 845
 Thr Val Gln Ala Glu Cys Glu Asn Arg Lys Ile Leu Asp Phe Pro Leu
 850 855 860
 Lys Tyr Arg Lys Met Thr Leu Met Phe Glu Lys Val Ser Thr Cys Phe
 865 870 875 880
 His Val Thr Leu Leu Lys Asp Tyr Met Val Phe Tyr Val Leu Asn Thr
 885 890 895
 Leu Asn Phe Ala Ser Arg Trp Pro Arg Arg Arg Arg Ala Ala Thr Ile
 900 905 910
 Pro Gln Pro Val Ile Pro Met Val Gln Val Pro Val Gln Val Pro Ile
 915 920 925
 Val Pro Ala Glu Asn Phe Asn Pro Asn Val Pro Pro Pro Pro Pro Pro
 930 935 940
 Pro Gln Gly Gln Pro Met Leu Val Asp Ser Ala Ile Gly Leu Leu Thr
 945 950 955 960
 Pro Ile Arg Pro Ile Leu Val Ala His Pro Gln Asn Val Val Ser Asn
 965 970 975
 Ser Leu Asp Lys Ile Val Asp Val Lys Glu Arg Ile Ser Glu Ala Gln
 980 985 990
 Gly Asn Ala Ser Glu Ala Glu Asn Ala His Leu Arg Met Glu Leu Arg
 995 1000 1005
 Met Ala Glu Ser Gln Met Ala His Leu Asp Pro Tyr Thr Lys Asn
 1010 1015 1020
 Asn Cys Leu Leu Arg Ala Leu Gln Gln Val Asp Met Glu Leu Gln
 1025 1030 1035

Gln Leu His Leu Asn Pro Thr Val Glu Gly
1040 1045

<210> 12
<211> 1999
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (86)..(1498)

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cgcccgctgcc ggccgctcgc ccgcc atg cct ggc ttc gac tac aag ttc ctg 112
Met Pro Gly Phe Asp Tyr Lys Phe Leu
1 5
gag aag ccc aag cga cgg ctg ctg tgc cca ctg tgc ggg aag ccc atg 160
Glu Lys Pro Lys Arg Arg Leu Leu Cys Pro Leu Cys Gly Lys Pro Met
10 15 20 25
cgc gag cct gtg cag gtt tcc acc tgc ggc cac cgt ttc tgc gat acc 208
Arg Glu Pro Val Gln Val Ser Thr Cys Gly His Arg Phe Cys Asp Thr
30 35 40
tgc ctg cag gag ttc ctc agt gaa gga gtc ttc aag tgc cct gag gac 256
Cys Leu Gln Glu Phe Leu Ser Glu Gly Val Phe Lys Cys Pro Glu Asp
45 50 55
cag ctt cct ctg gac tat gcc aag atc tac cca gac ccg gag ctg gaa 304
Gln Leu Pro Leu Asp Tyr Ala Lys Ile Tyr Pro Asp Pro Glu Leu Glu
60 65 70
gta caa gta ttg ggc ctg cct atc cgc tgc atc cac agt gag gag ggc 352
Val Gln Val Leu Gly Leu Pro Ile Arg Cys Ile His Ser Glu Glu Gly
75 80 85
tgc cgc tgg agt ggg cca cta cgt cat cta cag ggc cac ctg aat acc 400
Cys Arg Trp Ser Gly Pro Leu Arg His Leu Gln Gly His Leu Asn Thr
90 95 100 105
tgc agc ttc aat gtc att ccc tgc cct aat cgc tgc ccc atg aag ctg 448
Cys Ser Phe Asn Val Ile Pro Cys Pro Asn Arg Cys Pro Met Lys Leu
110 115 120
agc cgc cgt gat cta cct gca cac ttg cag cat gac tgc ccc aag cgg 496
Ser Arg Arg Asp Leu Pro Ala His Leu Gln His Asp Cys Pro Lys Arg
125 130 135
cgc ctc aag tgc gag ttt tgt ggc tgt gac ttc agt ggg gag gcc tat 544
Arg Leu Lys Cys Glu Phe Cys Gly Cys Asp Phe Ser Gly Glu Ala Tyr
140 145 150
gag agc cat gag ggt atg tgc ccc cag gag agt gtc tac tgt gag aat 592

Glu Ser His Glu Gly Met Cys Pro Gln Glu Ser Val Tyr Cys Glu Asn	
155	160 165
aag tgt ggt gcc cgc atg atg cgg ggg ctg ctg gcc cag cat gcc acc	640
Lys Cys Gly Ala Arg Met Met Arg Gly Leu Leu Ala Gln His Ala Thr	
170	175 180 185
tct gag tgc ccc aag cgc act cag ccc tgc acc tac tgc act aag gag	688
Ser Glu Cys Pro Lys Arg Thr Gln Pro Cys Thr Tyr Cys Thr Lys Glu	
	190 195 200
ttc gtc ttt gac acc atc cag agc cac cag tac cag tgc cca agg ctg	736
Phe Val Phe Asp Thr Ile Gln Ser His Gln Tyr Gln Cys Pro Arg Leu	
	205 210 215
cct gtt gcc tgc ccc aac caa tgt ggt gtg ggc act gtg gct cgg gag	784
Pro Val Ala Cys Pro Asn Gln Cys Gly Val Gly Thr Val Ala Arg Glu	
	220 225 230
gac ctg cca ggc cat ctg aag gac agc tgt aac acc gcc ctg gtg ctc	832
Asp Leu Pro Gly His Leu Lys Asp Ser Cys Asn Thr Ala Leu Val Leu	
	235 240 245
tgc cca ttc aaa gac tcc ggc tgc aag cac agg tgc cct aag ctg gca	880
Cys Pro Phe Lys Asp Ser Gly Cys Lys His Arg Cys Pro Lys Leu Ala	
	250 255 260 265
atg gca cgg cat gtg gag gag agt gtg aag cca cat ctg gcc atg atg	928
Met Ala Arg His Val Glu Glu Ser Val Lys Pro His Leu Ala Met Met	
	270 275 280
tgt gcc ctg gtg agc cgg caa cgg cag gag ctg cag gag ctt cgg cga	976
Cys Ala Leu Val Ser Arg Gln Arg Gln Glu Leu Gln Glu Arg Arg	
	285 290 295
gag ctg gag gag cta tca gtg ggc agt gat ggc gtg ctc atc tgg aag	1024
Glu Leu Glu Glu Leu Ser Val Gly Ser Asp Gly Val Leu Ile Trp Lys	
	300 305 310
att ggc agc tat gga cgg cgg cta cag gag gcc aag gcc aag ccc aac	1072
Ile Gly Ser Tyr Gly Arg Arg Leu Gln Glu Ala Lys Ala Lys Pro Asn	
	315 320 325
ctt gag tgc ttc agc cca gcc ttc tac aca cat aag tat ggt tac aag	1120
Leu Glu Cys Phe Ser Pro Ala Phe Tyr Thr His Lys Tyr Gly Tyr Lys	
	330 335 340 345
ctg cag gtg tct gca ttc ctc aat ggc aat ggc agt ggt gag ggc aca	1168
Leu Gln Val Ser Ala Phe Leu Asn Gly Asn Gly Ser Gly Glu Gly Thr	
	350 355 360
cac ctc tca ctg tac att cgt gtg ctg cct ggt gcc ttt gac aat ctc	1216
His Leu Ser Leu Tyr Ile Arg Val Leu Pro Gly Ala Phe Asp Asn Leu	
	365 370 375
ctt gag tgg ccc ttt gcc cgc cgt gtc acc ttc tcc ctg ctg gat cag	1264
Leu Glu Trp Pro Phe Ala Arg Arg Val Thr Phe Ser Leu Leu Asp Gln	

380	385	390	
agc gac cct ggg ctg gct aaa cca cag cac gtc act gag acc ttc cac			1312
Ser Asp Pro Gly Leu Ala Lys Pro Gln His Val Thr Glu Thr Phe His			
395	400	405	
ccc gac cca aac tgg aag aat ttc cag aag cca ggc acg tgg cgg ggc			1360
Pro Asp Pro Asn Trp Lys Asn Phe Gln Lys Pro Gly Thr Trp Arg Gly			
410	415	420	425
tcc ctg gat gag agt tct ctg ggc ttt ggt tat ccc aag ttc atc tcc			1408
Ser Leu Asp Glu Ser Ser Leu Gly Phe Gly Tyr Pro Lys Phe Ile Ser			
	430	435	440
cac cag gac att cga aag cga aac tat gtg cgg gat gat gca gtc ttc			1456
His Gln Asp Ile Arg Lys Arg Asn Tyr Val Arg Asp Asp Ala Val Phe			
	445	450	455
atc cgt gct gct gtt gaa ctg ccc cgg aag atc ctc agc tga			1498
Ile Arg Ala Ala Val Glu Leu Pro Arg Lys Ile Leu Ser			
	460	465	470
gtgcaggtgg ggttcgaggg gaaaggacga tggggcatga cctcagtcag gcactggctg			1558
aacttggaga gggggccgga cccccgtcag ctgcttctgc tgcctagggt ctgttacc			1618
atcctccctc cccagccac caccctcagg tgcctccaat tgggtgcttca gccctggccc			1678
ctgtggggaa caggtcttgg ggtcatgaag ggctggaaac aagtgacccc agggcctgtc			1738
tcccttcttg ggtagggcag acatgccttg gtgccggtca cactctacac ggactgaggt			1798
gcctgctcag gtgctatgtc ccaagagcca taagggggtg ggaattgggg agggagaaag			1858
ggtagttcaa agagtctgtc ttgagatctg attttttccc cctttaccta gctgtgcccc			1918
ctctgggttat ttatttcctt agtgccagga gggcacagca ggggagccct gattttta			1978
aatccggaa ttgtatttat t			1999

<210> 13
 <211> 470
 <212> PRT
 <213> Homo sapiens

<400> 13

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Leu	Cys	Pro	Leu	Cys	Gly	Lys	Pro	Met	Arg	Glu	Pro	Val	Gln	Val	Ser
		20					25						30		

Thr Cys Gly His Arg Phe Cys Asp Thr Cys Leu Gln Glu Phe Leu Ser

35

40

45

Glu Gly Val Phe Lys Cys Pro Glu Asp Gln Leu Pro Leu Asp Tyr Ala
50 55 60

Lys Ile Tyr Pro Asp Pro Glu Leu Glu Val Gln Val Leu Gly Leu Pro
65 70 75 80

Ile Arg Cys Ile His Ser Glu Glu Gly Cys Arg Trp Ser Gly Pro Leu
85 90 95

Arg His Leu Gln Gly His Leu Asn Thr Cys Ser Phe Asn Val Ile Pro
100 105 110

Cys Pro Asn Arg Cys Pro Met Lys Leu Ser Arg Arg Asp Leu Pro Ala
115 120 125

His Leu Gln His Asp Cys Pro Lys Arg Arg Leu Lys Cys Glu Phe Cys
130 135 140

Gly Cys Asp Phe Ser Gly Glu Ala Tyr Glu Ser His Glu Gly Met Cys
145 150 155 160

Pro Gln Glu Ser Val Tyr Cys Glu Asn Lys Cys Gly Ala Arg Met Met
165 170 175

Arg Gly Leu Leu Ala Gln His Ala Thr Ser Glu Cys Pro Lys Arg Thr
180 185 190

Gln Pro Cys Thr Tyr Cys Thr Lys Glu Phe Val Phe Asp Thr Ile Gln
195 200 205

Ser His Gln Tyr Gln Cys Pro Arg Leu Pro Val Ala Cys Pro Asn Gln
210 215 220

Cys Gly Val Gly Thr Val Ala Arg Glu Asp Leu Pro Gly His Leu Lys
225 230 235 240

Asp Ser Cys Asn Thr Ala Leu Val Leu Cys Pro Phe Lys Asp Ser Gly
245 250 255

Cys Lys His Arg Cys Pro Lys Leu Ala Met Ala Arg His Val Glu Glu
260 265 270

Ser Val Lys Pro His Leu Ala Met Met Cys Ala Leu Val Ser Arg Gln
275 280 285

Arg Gln Glu Leu Gln Glu Leu Arg Arg Glu Leu Glu Glu Leu Ser Val
290 295 300

Gly Ser Asp Gly Val Leu Ile Trp Lys Ile Gly Ser Tyr Gly Arg Arg
305 310 315 320

Leu Gln Glu Ala Lys Ala Lys Pro Asn Leu Glu Cys Phe Ser Pro Ala
325 330 335

Phe Tyr Thr His Lys Tyr Gly Tyr Lys Leu Gln Val Ser Ala Phe Leu
340 345 350

Asn Gly Asn Gly Ser Gly Glu Gly Thr His Leu Ser Leu Tyr Ile Arg
355 360 365

Val Leu Pro Gly Ala Phe Asp Asn Leu Leu Glu Trp Pro Phe Ala Arg
370 375 380

Arg Val Thr Phe Ser Leu Leu Asp Gln Ser Asp Pro Gly Leu Ala Lys
385 390 395 400

Pro Gln His Val Thr Glu Thr Phe His Pro Asp Pro Asn Trp Lys Asn
405 410 415

Phe Gln Lys Pro Gly Thr Trp Arg Gly Ser Leu Asp Glu Ser Ser Leu
420 425 430

Gly Phe Gly Tyr Pro Lys Phe Ile Ser His Gln Asp Ile Arg Lys Arg
435 440 445

Asn Tyr Val Arg Asp Asp Ala Val Phe Ile Arg Ala Ala Val Glu Leu
450 455 460

Pro Arg Lys Ile Leu Ser
465 470

<210> 14
<211> 1105
<212> DNA

<213> Caenorhabditis elegans

<220>

<221> CDS

<222> (10)..(1017)

<400> 14

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aac aac tca gat gac acg tcg ttc gct gcc gat cga tcg aac agt ctt	99
Asn Asn Ser Asp Asp Thr Ser Phe Ala Ala Asp Arg Ser Asn Ser Leu	
15 20 25 30	
ctg aat gcg acg tgc ccg gcg aga att caa aat tca gta gat caa cgg	147
Leu Asn Ala Thr Cys Pro Ala Arg Ile Gln Asn Ser Val Asp Gln Arg	
35 40 45	
aaa atc aat cga tca ttc aat gat tcg ctg tcg tcc gga tat agt gga	195
Lys Ile Asn Arg Ser Phe Asn Asp Ser Leu Ser Ser Gly Tyr Ser Gly	
50 55 60	
aaa tgg ctt cgt cca aag cgt gaa gcg ctc aag atc act cca ttg gct	243
Lys Trp Leu Arg Pro Lys Arg Glu Ala Leu Lys Ile Thr Pro Leu Ala	
65 70 75	
cag att gac gag gcg ccg gca act aaa aga cat agc tcg gcg aag gat	291
Gln Ile Asp Glu Ala Pro Ala Thr Lys Arg His Ser Ser Ala Lys Asp	
80 85 90	
aag cac aca gaa tac aaa acg cga ctt tgt gat gcg ttc cgc cgt gaa	339
Lys His Thr Glu Tyr Lys Thr Arg Leu Cys Asp Ala Phe Arg Arg Glu	
95 100 105 110	
gga tac tgc ccg tac aac gac aat tgc aca tat gct cac gga caa gat	387
Gly Tyr Cys Pro Tyr Asn Asp Asn Cys Thr Tyr Ala His Gly Gln Asp	
115 120 125	
gag ctg aga gtt ccg aga cgc cgc caa gag tat tat tcc cga gat cca	435
Glu Leu Arg Val Pro Arg Arg Arg Gln Glu Tyr Tyr Ser Arg Asp Pro	
130 135 140	
cca cgt gag cgc cgt gat tct cgt tct aga cga gac gac gtg gat aca	483
Pro Arg Glu Arg Arg Asp Ser Arg Ser Arg Arg Asp Asp Val Asp Thr	
145 150 155	
aca atc aat cga tcg agt tct tca gca tcg aag cat cat gat gag aat	531
Thr Ile Asn Arg Ser Ser Ser Ser Ala Ser Lys His His Asp Glu Asn	
160 165 170	
cgg aga ccc agc aac aac cac gga agc tcg aat cgt cgt cag att tgt	579
Arg Arg Pro Ser Asn Asn His Gly Ser Ser Asn Arg Arg Gln Ile Cys	
175 180 185 190	
cac aat ttc gag aga gga aac tgc aga tat ggt cca aga tgc cgc ttc	627
His Asn Phe Glu Arg Gly Asn Cys Arg Tyr Gly Pro Arg Cys Arg Phe	

195	200	205	
att cac gtc gaa caa atg caa cat ttc aat gcg aat gcg acg gtt tac Ile His Val Glu Gln Met Gln His Phe Asn Ala Asn Ala Thr Val Tyr 210 215 220			675
gcg cca cct tct tcc gat tgt ccg ccg ccg att gcc tac tac cat cat Ala Pro Pro Ser Ser Asp Cys Pro Pro Pro Ile Ala Tyr Tyr His His 225 230 235			723
cat cca caa cat cag caa caa ttc ctg cca ttt cca atg cca tat ttc His Pro Gln His Gln Gln Gln Phe Leu Pro Phe Pro Met Pro Tyr Phe 240 245 250			771
ttg gct cca ccg ccg caa gct caa caa gga gct cct ttt cca gtg caa Leu Ala Pro Pro Pro Gln Ala Gln Gln Gly Ala Pro Phe Pro Val Gln 255 260 265 270			819
tat att cca cag caa cat gat ttg atg aat agc cag cca atg tat gca Tyr Ile Pro Gln Gln His Asp Leu Met Asn Ser Gln Pro Met Tyr Ala 275 280 285			867
cca atg gca ccg aca tac tac tat caa cca att aat tcg aat ggc atg Pro Met Ala Pro Thr Tyr Tyr Tyr Gln Pro Ile Asn Ser Asn Gly Met 290 295 300			915
ccc atg atg gat gtg act att gat ccg aat gcc acg ggc ggt gcg ttt Pro Met Met Asp Val Thr Ile Asp Pro Asn Ala Thr Gly Gly Ala Phe 305 310 315			963
gaa gtg ttc ccc gat gga ttc ttc tct cag cca cca cca act att att Glu Val Phe Pro Asp Gly Phe Phe Ser Gln Pro Pro Pro Thr Ile Ile 320 325 330			1011
tcc taa ttttgccgta ttttccatat tttgttttgt atatttatcc actcaccccc Ser 335			1067
tctctttgtc ctgtgaatga acttgtgcc aaaaagcc			1105

<210> 15
 <211> 335
 <212> PRT
 <213> Caenorhabditis elegans

<400> 15

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Ser	Asp	Asp	Thr	Ser	Phe	Ala	Ala	Asp	Arg	Ser	Asn	Ser	Leu	Leu	Asn
	20							25					30		

Ala Thr Cys Pro Ala Arg Ile Gln Asn Ser Val Asp Gln Arg Lys Ile

Asn Arg Ser Phe Asn Asp Ser Leu Ser Ser Gly Tyr Ser Gly Lys Trp
 50 55 60

Leu Arg Pro Lys Arg Glu Ala Leu Lys Ile Thr Pro Leu Ala Gln Ile
 65 70 75 80

Asp Glu Ala Pro Ala Thr Lys Arg His Ser Ser Ala Lys Asp Lys His
 85 90 95

Thr Glu Tyr Lys Thr Arg Leu Cys Asp Ala Phe Arg Arg Glu Gly Tyr
 100 105 110

Cys Pro Tyr Asn Asp Asn Cys Thr Tyr Ala His Gly Gln Asp Glu Leu
 115 120 125

Arg Val Pro Arg Arg Arg Gln Glu Tyr Tyr Ser Arg Asp Pro Pro Arg
 130 135 140

Glu Arg Arg Asp Ser Arg Ser Arg Arg Asp Asp Val Asp Thr Thr Ile
 145 150 155 160

Asn Arg Ser Ser Ser Ser Ala Ser Lys His His Asp Glu Asn Arg Arg
 165 170 175

Pro Ser Asn Asn His Gly Ser Ser Asn Arg Arg Gln Ile Cys His Asn
 180 185 190

Phe Glu Arg Gly Asn Cys Arg Tyr Gly Pro Arg Cys Arg Phe Ile His
 195 200 205

Val Glu Gln Met Gln His Phe Asn Ala Asn Ala Thr Val Tyr Ala Pro
 210 215 220

Pro Ser Ser Asp Cys Pro Pro Pro Ile Ala Tyr Tyr His His His Pro
 225 230 235 240

Gln His Gln Gln Gln Phe Leu Pro Phe Pro Met Pro Tyr Phe Leu Ala
 245 250 255

Pro Pro Pro Gln Ala Gln Gln Gly Ala Pro Phe Pro Val Gln Tyr Ile
 260 265 270

Pro Gln Gln His Asp Leu Met Asn Ser Gln Pro Met Tyr Ala Pro Met
 275 280 285

Ala Pro Thr Tyr Tyr Tyr Gln Pro Ile Asn Ser Asn Gly Met Pro Met
 290 295 300

Met Asp Val Thr Ile Asp Pro Asn Ala Thr Gly Gly Ala Phe Glu Val
 305 310 315 320

Phe Pro Asp Gly Phe Phe Ser Gln Pro Pro Pro Thr Ile Ile Ser
 325 330 335

<210> 16
 <211> 2077
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (301)..(1614)

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 ttttattggt gcaatgcaat attcgcgga cgaataacaa caacatacat aactcaatat 120
 tcaagtgcaa agcaaataca aatcaaacac aaagaaaaag caacgaaata aagatatata 180
 gaaaagaaaa acaaaacgaa aaaattcgca cattttttct gtcttgtcca gtggaaaata 240
 caacaaataa acaacaacgg ctaaatacaag ttaacaatct gttcaaaacc aatcaacaaa 300
 atg tct gct gat att ctg cag aaa tca aga gag cag gat gat tgc cac 348
 Met Ser Ala Asp Ile Leu Gln Lys Ser Arg Glu Gln Asp Asp Ser His
 1 5 10 15
 tac ttc gag cgt ggc gat ata tcc aaa tac gta acg atg aac gat cac 396
 Tyr Phe Glu Arg Gly Asp Ile Ser Lys Tyr Val Thr Met Asn Asp His
 20 25 30
 ttg ggt gat ttc gat tgc aac gag gtg cgc aag gaa ata agg atg ctg 444
 Leu Gly Asp Phe Asp Cys Asn Glu Val Arg Lys Glu Ile Arg Met Leu
 35 40 45
 ctc gcc cac ggc gcc aac ttg gat cag cag cac cag cag cag cca cat 492
 Leu Ala His Gly Ala Asn Leu Asp Gln Gln His Gln Gln Gln Pro His
 50 55 60
 cgc cac cat ggc ggt ctc aca cgc acc att tca cag ccg gcc cag ctc 540
 Arg His His Gly Gly Leu Thr Arg Thr Ile Ser Gln Pro Ala Gln Leu
 65 70 75 80

atc cag cag cag cag cag caa cac caa cag cag cag cag cag cag cag	588
Ile Gln Gln Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln	
85 90 95	
cca cct gtt gcc agt ctg gtg acc atc acc gag aac ctg ggc aac atg	636
Pro Pro Val Ala Ser Leu Val Thr Ile Thr Glu Asn Leu Gly Asn Met	
100 105 110	
aac ctg cac cga aag ctg gag cga acc caa tcg gag cca ctg ccg cca	684
Asn Leu His Arg Lys Leu Glu Arg Thr Gln Ser Glu Pro Leu Pro Pro	
115 120 125	
cag cag ccg atg aac aca tcc aga tac aag acc gag ctg tgc cgt ccg	732
Gln Gln Pro Met Asn Thr Ser Arg Tyr Lys Thr Glu Leu Cys Arg Pro	
130 135 140	
ttc gag gag gcc gga gaa tgc aag tac ggc gag aag tgc cag ttc gcc	780
Phe Glu Glu Ala Gly Glu Cys Lys Tyr Gly Glu Lys Cys Gln Phe Ala	
145 150 155 160	
cat gga agc cat gag ttg cga aac gtg cac cgt cat ccc aag tac aag	828
His Gly Ser His Glu Leu Arg Asn Val His Arg His Pro Lys Tyr Lys	
165 170 175	
acg gaa tac tgc cgc acc ttc cac agc gtg ggc ttc tgt ccc tac gga	876
Thr Glu Tyr Cys Arg Thr Phe His Ser Val Gly Phe Cys Pro Tyr Gly	
180 185 190	
ccg cgc tgt cac ttt gtt cac aat gcg gac gag gcc cgc gcc caa cag	924
Pro Arg Cys His Phe Val His Asn Ala Asp Glu Ala Arg Ala Gln Gln	
195 200 205	
gcg gcc cag gca gcc aag tcc tcc acc cag tcg cag tcg cag tcg cag	972
Ala Ala Gln Ala Ala Lys Ser Ser Thr Gln Ser Gln Ser Gln Ser Gln	
210 215 220	
cag tcg tcg tcg cag aac ttc tcg ccg aag agc aac cag agc agc aat	1020
Gln Ser Ser Ser Gln Asn Phe Ser Pro Lys Ser Asn Gln Ser Ser Asn	
225 230 235 240	
caa agt agc aac agt agc agc agc agc agc agc agc ggc ggc ggc ggt	1068
Gln Ser Ser Asn Ser Ser Ser Ser Ser Ser Ser Ser Gly Gly Gly Gly	
245 250 255	
ggc ggc ggc aac agc atc aac aac aac aac ggt agc caa ttc tat ctg	1116
Gly Gly Gly Asn Ser Ile Asn Asn Asn Asn Asn Gly Ser Gln Phe Tyr Leu	
260 265 270	
ccg cta agc cca ccg ctg agc atg agc aca gga tcg gac cgg gaa tcg	1164
Pro Leu Ser Pro Pro Leu Ser Met Ser Thr Gly Ser Asp Arg Glu Ser	
275 280 285	
ccc acc gga tca ctg tcc ctc agc ccc acc aac tcg ttg acc agc ttc	1212
Pro Thr Gly Ser Leu Ser Leu Ser Pro Thr Asn Ser Leu Thr Ser Phe	
290 295 300	

ccg ttc cac gat gcc ctg cag cat gga tat ttg gca tcg aat ggc gcc Pro Phe His Asp Ala Leu Gln His Gly Tyr Leu Ala Ser Asn Gly Ala 305 310 315 320	1260
aag agc aac agt tcc gcc tcg tcc aca tca tcg gcc tct gga atg ggt Lys Ser Asn Ser Ser Ala Ser Ser Thr Ser Ser Ala Ser Gly Met Gly 325 330 335	1308
ctg ggc atg agc atg ggc atc ggc cag ggc atg atc atc ggt cag ggt Leu Gly Met Ser Met Gly Ile Gly Gln Gly Met Ile Ile Gly Gln Gly 340 345 350	1356
ttg gga atg gga cat cat gga ccg gcc aca ccg ccg gag agc ccc aat Leu Gly Met Gly His His Gly Pro Ala Thr Pro Pro Glu Ser Pro Asn 355 360 365	1404
gtg ccc ata tcg cca gtg cat aca cca cca ccg tac gat gtg gtg gtc Val Pro Ile Ser Pro Val His Thr Pro Pro Pro Tyr Asp Val Val Val 370 375 380	1452
agt gga tct gga gcg ggc aac aat agc gtt ggc agc aag cag ctc ctg Ser Gly Ser Gly Ala Gly Asn Asn Ser Val Gly Ser Lys Gln Leu Leu 385 390 395 400	1500
cag aag agc gtc agc aca ccg atg cag cag gag gat acg ccc agg ttg Gln Lys Ser Val Ser Thr Pro Met Gln Gln Glu Asp Thr Pro Arg Leu 405 410 415	1548
ccg gtt ttc aac cgt ctc agc tcc ggt gtg gag gcc tac cag cag cag Pro Val Phe Asn Arg Leu Ser Ser Gly Val Glu Ala Tyr Gln Gln Gln 420 425 430	1596
tcc aat ttg gga ctc taa acgcgtggca gtctgcgaaa caaaattgaa Ser Asn Leu Gly Leu 435	1644
ttgaaacacc atccagcatc caactcacgc ccattccaagc atccctccat caacaaacca	1704
gcatccttga caaaatctca gtaacgacca aaccatggaa actgaaaaca aaactactct	1764
cgcagtccaa tttgaaacgc aaatatgcca aggcaaatgg atttccggtg gcgtaacttc	1824
gttgacagaat aagtgtgtat caagtatacg ccaaacacag acacccctta attatgaacc	1884
gaccccttgat atcaattctc tcattgctgt gacagtcaaa cgtaatcggt atacaataat	1944
cggtatatga gaaggaccga attacggact actacgggac aattagttag atagatacgt	2004
aaatgacaaa caaacaatcc aagcaaacga tgatcttaaa ctataactaa atactaaaaa	2064
ctaaaaacta aca	2077

<210> 17
 <211> 437
 <212> PRT
 <213> Drosophila melanogaster

<400> 17

Met Ser Ala Asp Ile Leu Gln Lys Ser Arg Glu Gln Asp Asp Ser His
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Tyr Phe Glu Arg Gly Asp Ile Ser Lys Tyr Val Thr Met Asn Asp His
20 25 30

Leu Gly Asp Phe Asp Cys Asn Glu Val Arg Lys Glu Ile Arg Met Leu
35 40 45

Leu Ala His Gly Ala Asn Leu Asp Gln Gln His Gln Gln Gln Pro His
50 55 60

Arg His His Gly Gly Leu Thr Arg Thr Ile Ser Gln Pro Ala Gln Leu
65 70 75 80

Ile Gln Gln Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln
85 90 95

Pro Pro Val Ala Ser Leu Val Thr Ile Thr Glu Asn Leu Gly Asn Met
100 105 110

Asn Leu His Arg Lys Leu Glu Arg Thr Gln Ser Glu Pro Leu Pro Pro
115 120 125

Gln Gln Pro Met Asn Thr Ser Arg Tyr Lys Thr Glu Leu Cys Arg Pro
130 135 140

Phe Glu Glu Ala Gly Glu Cys Lys Tyr Gly Glu Lys Cys Gln Phe Ala
145 150 155 160

His Gly Ser His Glu Leu Arg Asn Val His Arg His Pro Lys Tyr Lys
165 170 175

Thr Glu Tyr Cys Arg Thr Phe His Ser Val Gly Phe Cys Pro Tyr Gly
180 185 190

Pro Arg Cys His Phe Val His Asn Ala Asp Glu Ala Arg Ala Gln Gln
195 200 205

Ala Ala Gln Ala Ala Lys Ser Ser Thr Gln Ser Gln Ser Gln Ser Gln
210 215 220

Gln Ser Ser Ser Gln Asn Phe Ser Pro Lys Ser Asn Gln Ser Ser Asn
 225 230 235 240

Gln Ser Ser Asn Ser Ser Ser Ser Ser Ser Ser Gly Gly Gly Gly
 245 250 255

Gly Gly Gly Asn Ser Ile Asn Asn Asn Asn Gly Ser Gln Phe Tyr Leu
 260 265 270

Pro Leu Ser Pro Pro Leu Ser Met Ser Thr Gly Ser Asp Arg Glu Ser
 275 280 285

Pro Thr Gly Ser Leu Ser Leu Ser Pro Thr Asn Ser Leu Thr Ser Phe
 290 295 300

Pro Phe His Asp Ala Leu Gln His Gly Tyr Leu Ala Ser Asn Gly Ala
 305 310 315 320

Lys Ser Asn Ser Ser Ala Ser Ser Thr Ser Ser Ala Ser Gly Met Gly
 325 330 335

Leu Gly Met Ser Met Gly Ile Gly Gln Gly Met Ile Ile Gly Gln Gly
 340 345 350

Leu Gly Met Gly His His Gly Pro Ala Thr Pro Pro Glu Ser Pro Asn
 355 360 365

Val Pro Ile Ser Pro Val His Thr Pro Pro Pro Tyr Asp Val Val Val
 370 375 380

Ser Gly Ser Gly Ala Gly Asn Asn Ser Val Gly Ser Lys Gln Leu Leu
 385 390 395 400

Gln Lys Ser Val Ser Thr Pro Met Gln Gln Glu Asp Thr Pro Arg Leu
 405 410 415

Pro Val Phe Asn Arg Leu Ser Ser Gly Val Glu Ala Tyr Gln Gln Gln
 420 425 430

Ser Asn Leu Gly Leu
 435

<210> 18
 <211> 3922
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (774)..(1733)

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 gaacttaggg caaagagttt ttttttcagg aatcacatcc ctgtctcccc caacctcaga 180
 ccaggccccc aatctctccc ccacaagaaa aagcaaaggc agtctgaaaa cctgttgcca 240
 aaggaaggga acattctga aggaggaagt tgagagtctt aggccaggtc ttgaaggagg 300
 gggatatcaat taagcagaga ctgattggaa ggggacctaa cgtgcctatg atagactcct 360
 ttctgaggtt tacctgtttt tgtcgcgggc ggtggcgggg cggtgcggt aatctagaga 420
 ggtctgggtt gtgtgagata ttttgagttg aagaatctat ttgactagta aaaaagttga 480
 actttaaaagt ggtagctttg gggacagagg acatgggggt tgcattgcag gagtcagcat 540
 ggagcagggt gcttgtcaca cagtttgat cttgtggtt cttacgcagtg gggccaaaat 600
 aaaccaggt gaatggccta tgggagggag agaggaagg gagcttgcta gagccgaggt 660
 agagatgagt tctttgagaa agagcgggcg tttgtgattg ttagggggc tgcccatagt 720
 ggacatcctg gtggatgtcc tctgtcctta ccatecttct cttctctctc cag ggt 776
 Gly
 1
 aac aag atg ctc aac tat agt gct ccc agt gca ggg ggt tgc ctg ctg 824
 Asn Lys Met Leu Asn Tyr Ser Ala Pro Ser Ala Gly Gly Cys Leu Leu
 5 10 15
 gac aga aag gca gtg ggc acc cct gct ggt ggg ggc ttc cct cgg agg 872
 Asp Arg Lys Ala Val Gly Thr Pro Ala Gly Gly Gly Phe Pro Arg Arg
 20 25 30
 cac tca gtc acc ctg ccc agc tcc aag ttc cac cag aac cag ctc ctc 920
 His Ser Val Thr Leu Pro Ser Ser Lys Phe His Gln Asn Gln Leu Leu
 35 40 45
 agc agc ctc aag ggt gag cca gcc ccc gct ctg agc tcg cga gac agc 968
 Ser Ser Leu Lys Gly Glu Pro Ala Pro Ala Leu Ser Ser Arg Asp Ser
 50 55 60 65
 cgc ttc cga gac cgc tcc ttc tcg gaa ggg ggc gag cgg ctg ctg ccc 1016
 Arg Phe Arg Asp Arg Ser Phe Ser Glu Gly Gly Glu Arg Leu Leu Pro

70	75	80	
acc cag aag cag ccc ggg ggc ggc cag gtc aac tcc agc cgc tac aag Thr Gln Lys Gln Pro Gly Gly Gly Gln Val Asn Ser Ser Arg Tyr Lys 85 90 95			1064
acg gag ctg tgc cgc ccc ttt gag gaa aac ggt gcc tgt aag tac ggg Thr Glu Leu Cys Arg Pro Phe Glu Glu Asn Gly Ala Cys Lys Tyr Gly 100 105 110			1112
gac aag tgc cag ttc gca cac ggc atc cac gag ctc cgc agc ctg acc Asp Lys Cys Gln Phe Ala His Gly Ile His Glu Leu Arg Ser Leu Thr 115 120 125			1160
cgc cac ccc aag tac aag acg gag ctg tgc cgc acc ttc cac acc atc Arg His Pro Lys Tyr Lys Thr Glu Leu Cys Arg Thr Phe His Thr Ile 130 135 140 145			1208
ggc ttt tgc ccc tac ggg ccc cgc tgc cac ttc atc cac aac gct gaa Gly Phe Cys Pro Tyr Gly Pro Arg Cys His Phe Ile His Asn Ala Glu 150 155 160			1256
gag cgc cgt gcc ctg gcc ggg gcc cgg gac ctc tcc gct gac cgt ccc Glu Arg Arg Ala Leu Ala Gly Ala Arg Asp Leu Ser Ala Asp Arg Pro 165 170 175			1304
cgc ctc cag cat agc ttt agc ttt gct ggg ttt ccc agt gcc gct gcc Arg Leu Gln His Ser Phe Ser Phe Ala Gly Phe Pro Ser Ala Ala Ala 180 185 190			1352
acc gcc gct gcc acc ggg ctg ctg gac agc ccc acg tcc atc acc cca Thr Ala Ala Ala Thr Gly Leu Leu Asp Ser Pro Thr Ser Ile Thr Pro 195 200 205			1400
ccc cct att ctg agc gcc gat gac ctc ctg ggc tca cct acc ctg ccc Pro Pro Ile Leu Ser Ala Asp Asp Leu Leu Gly Ser Pro Thr Leu Pro 210 215 220 225			1448
gat ggc acc aat aac cct ttt gcc ttc tcc agc cag gag ctg gca agc Asp Gly Thr Asn Asn Pro Phe Ala Phe Ser Ser Gln Glu Leu Ala Ser 230 235 240			1496
ctc ttt gcc cct agc atg ggg ctg ccc ggg ggt ggc tcc ccg acc acc Leu Phe Ala Pro Ser Met Gly Leu Pro Gly Gly Gly Ser Pro Thr Thr 245 250 255			1544
ttc ctc ttc cgg ccc atg tcc gag tcc cct cac atg ttt gac tct ccc Phe Leu Phe Arg Pro Met Ser Glu Ser Pro His Met Phe Asp Ser Pro 260 265 270			1592
ccc agc cct cag gat tct ctc tgc gac cag gag ggc tac ctg agc agc Pro Ser Pro Gln Asp Ser Leu Ser Asp Gln Glu Gly Tyr Leu Ser Ser 275 280 285			1640
tcc agc agc agc cac agt ggc tca gac tcc ccg acc ttg gac aac tca Ser Ser Ser Ser His Ser Gly Ser Asp Ser Pro Thr Leu Asp Asn Ser 290 295 300 305			1688

aga cgc ctg ccc atc ttc agc aga ctt tcc atc tca gat gac taa	1733
Arg Arg Leu Pro Ile Phe Ser Arg Leu Ser Ile Ser Asp Asp	
310 315	
gccagggtag ggagggacct cctgcctact ccagccccta cctgcaccc acatcccata	1793
ccctcttctc cctaccatc ccattcccca caggccctac attaacaagg ttaagctcaa	1853
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aaaaaaaaa tgagagaaaa gctaaaaaaaa aaaaagtaag gggtgagcag ttaatggtat	2693
tcattccaca tacaatatct gtgtaaaacg atttcctgta gaagtagctt taatggtttt	2753
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caatataaaa aagcttattt aacttatcaa aacgtattta ttgccaaact atgctttttt	2933
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cagttttaat atattattct tcaacgacat tttttgtaac ttacacttt tttgggttatt	3113
ttattttaaa aaaatgaaaa attaatttaa aaaaatgcaa aaaactgttg gattatttat	3173
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cacaactagg actgagaatg tatgtaaaag ttctgtgaca gtacagaagg aaaacaactt	3293

tttatgtata gcttctaaaa ggggaaaaaa aaaaaaaga gaaacccttt gacttccacg 3353
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 tccaatgtta atgtaaacag aactggcaca cacacattaa gatgaatgta attattattc 3473
 ctcttgctgg tcactaccgt cgctttctat ttctctttct ttgtgtgaat ttatttaaaa 3533
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 ggcccagcct tgccgacact tgtgtggcc 3922

<210> 19
 <211> 319
 <212> PRT
 <213> Homo sapiens

<400> 19

Gly Asn Lys Met Leu Asn Tyr Ser Ala Pro Ser Ala Gly Gly Cys Leu
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Leu Asp Arg Lys Ala Val Gly Thr Pro Ala Gly Gly Gly Phe Pro Arg
 20 25 30

Arg His Ser Val Thr Leu Pro Ser Ser Lys Phe His Gln Asn Gln Leu
 35 40 45

Leu Ser Ser Leu Lys Gly Glu Pro Ala Pro Ala Leu Ser Ser Arg Asp
 50 55 60

Ser Arg Phe Arg Asp Arg Ser Phe Ser Glu Gly Gly Glu Arg Leu Leu
 65 70 75 80

Pro Thr Gln Lys Gln Pro Gly Gly Gly Gln Val Asn Ser Ser Arg Tyr
 85 90 95

Lys Thr Glu Leu Cys Arg Pro Phe Glu Glu Asn Gly Ala Cys Lys Tyr
 100 105 110

Gly Asp Lys Cys Gln Phe Ala His Gly Ile His Glu Leu Arg Ser Leu
 115 120 125

Thr Arg His Pro Lys Tyr Lys Thr Glu Leu Cys Arg Thr Phe His Thr
 130 135 140

Ile Gly Phe Cys Pro Tyr Gly Pro Arg Cys His Phe Ile His Asn Ala
 145 150 155 160

Glu Glu Arg Arg Ala Leu Ala Gly Ala Arg Asp Leu Ser Ala Asp Arg
 165 170 175

Pro Arg Leu Gln His Ser Phe Ser Phe Ala Gly Phe Pro Ser Ala Ala
 180 185 190

Ala Thr Ala Ala Ala Thr Gly Leu Leu Asp Ser Pro Thr Ser Ile Thr
 195 200 205

Pro Pro Pro Ile Leu Ser Ala Asp Asp Leu Leu Gly Ser Pro Thr Leu
 210 215 220

Pro Asp Gly Thr Asn Asn Pro Phe Ala Phe Ser Ser Gln Glu Leu Ala
 225 230 235 240

Ser Leu Phe Ala Pro Ser Met Gly Leu Pro Gly Gly Gly Ser Pro Thr
 245 250 255

Thr Phe Leu Phe Arg Pro Met Ser Glu Ser Pro His Met Phe Asp Ser
 260 265 270

Pro Pro Ser Pro Gln Asp Ser Leu Ser Asp Gln Glu Gly Tyr Leu Ser
 275 280 285

Ser Ser Ser Ser Ser His Ser Gly Ser Asp Ser Pro Thr Leu Asp Asn
 290 295 300

Ser Arg Arg Leu Pro Ile Phe Ser Arg Leu Ser Ile Ser Asp Asp
 305 310 315

<210> 20
 <211> 1510
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (427)..(1404)

<400> 20

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cttttagggg ctgtgccaat ggcacccaaa tttttcttct ttctttttcg ctcgtattct	180
ctcacgtctt tgatcagtgt gagcagttac taatatactg gatcagagaa cattaactca	240
aagggtgata gtgtagatca ttggacatag tgtgacgggt ttgcactctt gttgcgcttg	300
ctctcttaac aagtcacatc ttatttagcc tcttcaccca taagttgatt gtaaagccgt	360
agaaccctat atcacagtct cttcggcaac tcaaccaata agaactatta aggattaaca	420
ctagcc atg atg ccg aat gtt gct cca aac agc tac tat tta aac ata	468
Met Met Pro Asn Val Ala Pro Asn Ser Tyr Tyr Leu Asn Ile	
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Pro Asn Ala Asn Ser Thr Ser Thr Thr Ser Ser Ile Phe Ser Asp	
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Leu Asn Lys Glu Tyr Glu Ser Lys Ile Lys Glu Ile Glu Glu Tyr Tyr	
35 40 45	
ata aag aca ctg ctc aat gaa aat acc gat aat gat gac agc agc agc	612
Ile Lys Thr Leu Leu Asn Glu Asn Thr Asp Asn Asp Asp Ser Ser Ser	
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tcc gag ggg cat aat ata aat gaa acg gac att tta agt gaa tac tca	660
Ser Glu Gly His Asn Ile Asn Glu Thr Asp Ile Leu Ser Glu Tyr Ser	
65 70 75	
cca agg cct tct cct tgg tta cca tcc aaa cca aac tgt tat cat ccg	708
Pro Arg Pro Ser Pro Trp Leu Pro Ser Lys Pro Asn Cys Tyr His Pro	
80 85 90	
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Leu Gly Asp Phe Lys Asp Leu Ile Ile Ser Asp Ser Arg Pro Thr Asn	
95 100 105 110	
aca tta cct att aat aac cct ttc gca ggc aat aat aac atc tca aca	804
Thr Leu Pro Ile Asn Asn Pro Phe Ala Gly Asn Asn Asn Ile Ser Thr	
115 120 125	
ctt gct aca act gag aaa aaa cgt aag aaa agg tca ctc gaa gtt aga	852
Leu Ala Thr Thr Glu Lys Lys Arg Lys Lys Arg Ser Leu Val Arg	
130 135 140	
gtt aac cct act tac acg aca agt gca ttt tca tta ccc ctg aca gcg	900

Val Asn Pro Thr Tyr Thr Thr Ser Ala Phe Ser Leu Pro Leu Thr Ala	
145 150 155	
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Glu Asn Leu Gln Lys Leu Ser Gln Val Asp Ser Gln Ser Thr Gly Leu	
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cca tac aca ctt cca att cag aaa aca aca aaa ctg gaa cct tgt aga	996
Pro Tyr Thr Leu Pro Ile Gln Lys Thr Thr Lys Leu Glu Pro Cys Arg	
175 180 185 190	
agg gca cct ttg cag ctt cct caa tta gtc aat aag acc tta tac aaa	1044
Arg Ala Pro Leu Gln Leu Pro Gln Leu Val Asn Lys Thr Leu Tyr Lys	
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act gag ctc tgt gaa tct ttt act att aaa ggc tat tgt aag tat gga	1092
Thr Glu Leu Cys Glu Ser Phe Thr Ile Lys Gly Tyr Cys Lys Tyr Gly	
210 215 220	
aat aaa tgc caa ttt gct cat ggt ctt aat gaa ctg aaa ttc aag aaa	1140
Asn Lys Cys Gln Phe Ala His Gly Leu Asn Glu Leu Lys Phe Lys Lys	
225 230 235	
aaa tca aac aat tat aga act aaa cct tgc ata aat tgg tcg aag tta	1188
Lys Ser Asn Asn Tyr Arg Thr Lys Pro Cys Ile Asn Trp Ser Lys Leu	
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ggc tac tgt ccg tac ggt aag cgt tgc tgt ttc aaa cac ggt gat gat	1236
Gly Tyr Cys Pro Tyr Gly Lys Arg Cys Cys Phe Lys His Gly Asp Asp	
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aag gac gtt gaa ata tat caa aat gct aac gat gga aga agt aag gat	1284
Lys Asp Val Glu Ile Tyr Gln Asn Ala Asn Asp Gly Arg Ser Lys Asp	
275 280 285	
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Thr Ala Leu Thr Pro Leu Pro Thr Ser Leu Ala Pro Ser Asn Asn Asp	
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Asn Ile Thr Asn Leu Ser Lys Pro Arg Asn Leu His Thr Ser Val Lys	
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Ala Leu Gln Arg Met Thr Trp	
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Lys Glu Tyr Glu Ser Lys Ile Lys Glu Ile Glu Glu Tyr Tyr Ile Lys
35 40 45

Thr Leu Leu Asn Glu Asn Thr Asp Asn Asp Asp Ser Ser Ser Ser Glu
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Gly His Asn Ile Asn Glu Thr Asp Ile Leu Ser Glu Tyr Ser Pro Arg
65 70 75 80

Pro Ser Pro Trp Leu Pro Ser Lys Pro Asn Cys Tyr His Pro Leu Gly
85 90 95

Asp Phe Lys Asp Leu Ile Ile Ser Asp Ser Arg Pro Thr Asn Thr Leu
100 105 110

Pro Ile Asn Asn Pro Phe Ala Gly Asn Asn Asn Ile Ser Thr Leu Ala
115 120 125

Thr Thr Glu Lys Lys Arg Lys Lys Arg Ser Leu Glu Val Arg Val Asn
130 135 140

Pro Thr Tyr Thr Thr Ser Ala Phe Ser Leu Pro Leu Thr Ala Glu Asn
145 150 155 160

Leu Gln Lys Leu Ser Gln Val Asp Ser Gln Ser Thr Gly Leu Pro Tyr
165 170 175

Thr Leu Pro Ile Gln Lys Thr Thr Lys Leu Glu Pro Cys Arg Arg Ala
180 185 190

Pro Leu Gln Leu Pro Gln Leu Val Asn Lys Thr Leu Tyr Lys Thr Glu
195 200 205

Leu Cys Glu Ser Phe Thr Ile Lys Gly Tyr Cys Lys Tyr Gly Asn Lys
210 215 220

Cys Gln Phe Ala His Gly Leu Asn Glu Leu Lys Phe Lys Lys Lys Ser
225 230 235 240

Asn Asn Tyr Arg Thr Lys Pro Cys Ile Asn Trp Ser Lys Leu Gly Tyr
245 250 255

Cys Pro Tyr Gly Lys Arg Cys Cys Phe Lys His Gly Asp Asp Lys Asp
260 265 270

Val Glu Ile Tyr Gln Asn Ala Asn Asp Gly Arg Ser Lys Asp Thr Ala
275 280 285

Leu Thr Pro Leu Pro Thr Ser Leu Ala Pro Ser Asn Asn Asp Asn Ile
290 295 300

Thr Asn Leu Ser Lys Pro Arg Asn Leu His Thr Ser Val Lys Ala Leu
305 310 315 320

Gln Arg Met Thr Trp
325